A M E N D M E N T S

Please amend the subject application as set forth below.

In the Claims

Cancel without prejudice claims 51 through 54 inclusive, claims 56 through 74 inclusive, 77, 83, 84, 88 through 90 inclusive, 99, 101, and 103 through 105 inclusive. Amend claims 79, 85 through 87 inclusive, 94, 96, 97, 100 and 102 as set forth below to insert underlined material and delete material which is either stricken through or enclosed in square brackets and stricken through. Add the following new claims 106 through 115 inclusive.

Pursuant to 37 CFR 1.121, a complete listing of all the claims of the subject application is set out below.

Claims 1 – 74 (Cancelled without prejudice)

75. (Previously presented) A method of determining the genotype at a locus within genetic material obtained from a biological sample, the method comprising:

A. reacting the material at the locus to produce a first reaction value indicative of the presence of a given allele at the locus;

B. forming a data set including the first reaction value;

C. establishing a distribution set of probability distributions, including at least one distribution, associating hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

D. applying the first reaction value to each pertinent probability distribution to determine a measure of a conditional probability of each genotype of interest at the locus; and

E. determining the genotype based on the data obtained from step (D).

76. (Previously presented) A method according to claim 75, wherein the distribution set includes a plurality of probability distributions for a corresponding plurality of genotypes of interest.

Claim 77 (Cancelled without prejudice)

78. (Previously presented) A method according to claim 76, further comprising:

(i) reacting the material at the locus to produce a second reaction value;

(ii) applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and

(iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

79. (Currently amended) A method according to claim 77 78, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

80. (Previously presented) A method according to claim 75, wherein:

step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

step (C) includes the step of using the reaction values in the data set to establish the probability distributions;

the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

81.   (Previously presented) A method, according to claim 80, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

(i) performing step (A) with respect to the locus of material obtained from each sample;

(ii) in step (B), including in the data set reaction values obtained from each sample.

82.   (Previously presented) A method according to claim 80, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

(i) performing step (A) at each of the selected loci;

(ii) in step (B), including in the data set reaction values obtained from each of the selected loci.

Claims 83 and 84 (Cancelled without prejudice)

85.   (Currently amended) A method according to claim 75, wherein step (E) further includes the step of calculating a confidence score, associated with the determination of the genotype being determined in step (E), based on data obtained from step (D).

86. (Currently amended) A method according to claim 80, wherein step (E) further includes the step of calculating a confidence score, associated with the <u>determination of the</u> genotype ~~being determined~~ <u>in step (E)</u>, based on data from step (D), the method further comprising:

(F) determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

87. (Currently amended) A method according to claim 75, wherein each allele is <u>defined by</u> a single specific nucleotide.

Claims 88 – 90 (Cancelled without prejudice)

91. (Previously presented) A method according to claim 78, wherein step (B) includes the step of including in the data set reaction values from prior tests at the locus obtained under comparable conditions.

92. (Previously presented) A method according to claim 82, wherein the loci are selected on the basis of their ability to discriminate among subjects.

93. (Previously presented) A method, according to claim 77, wherein the step A' of reacting the material involves using a different reaction from that of step A and the second allele is different from the given allele.

94. (Currently amended) A method according to claim 75, wherein step (A) includes the step of assaying for the given allele using genetic bit analysis, <u>allele-specific hybridization,</u> <u>or</u> allele-specific amplification, <u>including such amplification by a</u> polymerase chain reaction[,] or a ligase chain reaction.

95. (Previously presented) A method according to claim 82, wherein the loci are proximal to one another, so that the set of genotypes so produced may indicate a sequence of nucleotides associated with the genetic material.

96. (Currently amended) A method of associating with a sample of genetic material one of a predetermined plurality of genotypic[-class identifiers] classes defined with respect to a genetic locus sited in the genetic material together with a corresponding confidence measure, each genotypic[-class identifier] class identifying either a genotype defined with respect to the genetic locus or a failed-experiment condition, each genotype being defined by the identity of one or more alleles defined with respect to the genetic locus, the method comprising the steps of:

(a) carrying out one or more allele-sensitive reactions on the genetic material of the sample at the genetic locus to obtain a plurality of quantitative allele-indicative reaction values, each allele-indicative reaction value being indicative of the likely presence or absence of a particular allele defined with respect to the genetic locus, the plurality of reaction values corresponding to the sample being assembled as a reaction-value data point;

(b) obtaining with respect to each of the genotypic[-class identifiers] classes corresponding reaction-value data-point conditional-probability-measure distribution information providing, over a set of hypothetical reaction-value data points, a conditional probability measure as a function of the reaction values of each hypothetical reaction-value data point given the genotypic[-class identifier] class;

(c) evaluating for each of the genotypic[-class identifiers] classes the corresponding reaction-value data-point conditional-probability-measure distribution information with respect to the allele-indicative reaction values of the reaction-value

data point corresponding to the sample to obtain for each of the corresponding genotypic[-class identifiers] classes a reaction-value data-point conditional probability measure of the reaction-value data point given the genotypic[-class identifier] class;

(d) establishing with respect to each genotypic[-class identifier] class a [class-identifier] genotypic-class conditional probability measure of the genotypic[-class identifier] class given the reaction-value data point corresponding to the sample from the reaction-value data-point conditional probability measure of the reaction-value data point given the genotypic[-class identifier] class to obtain a set of [class-identifier] genotypic-class conditional probability measures of the respective genotypic[-class identifiers] classes given the reaction-value data point;

(e) selecting a highest-probability [class-identifier] genotypic-class conditional probability measure of a genotypic[-class identifier] class given the reaction-value data point having a highest probability value from the set of [class-identifier] genotypic-class conditional probabilities to identify a most-likely genotypic[-class identifier] class corresponding to said highest-probability [class-identifier] genotypic-class conditional probability measure for association with the sample; and

(f) establishing a confidence measure for the association of the most-likely genotypic[-class identifier] class with the sample, the confidence measure being established from values of the [class-identifier] genotypic-class conditional probability measures of the respective genotypic[-class identifiers] classes given the reaction-value data point corresponding to the sample.

97. (Currently amended) The method according to claim 96 in which at least one genotypic [~~class identifier~~] <u>class</u> identifies a failed-experiment condition.

98. (Previously presented) The method according to claim 96 in which the confidence measure is an LOD score.

Claim 99 (Cancelled without prejudice)

100. (Currently amended) The method according to claim 96 in which the allele-indicative reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, <u>allele-specific</u> hybridization, <u>and</u> allele-specific amplification<u>, including such amplification by a polymerase chain reaction</u> ~~and~~ <u>or</u> a ligase chain reaction.

Claim 101 (Cancelled without prejudice)

102. (Currently amended) The method according to claim ~~96~~ <u>98</u>, further comprising the step of triggering an alarm condition upon detecting a statistically significant downward trend in confidence scores over time.

Claims 103 – 105 (Cancelled without prejudice)

106. (new) A method of associating with a sample of genetic material (i) one of a predetermined plurality of genotypic classes defined with respect to a genetic locus sited in the genetic material and (ii) a confidence measure for the association of said genotypic class with the sample, each genotypic class identifying either a genotype defined with respect to the genetic locus or a failed-experiment condition, each genotype being defined by the identity of one or more alleles defined with respect to the genetic locus, the method comprising the steps of:

(a) carrying out one or more allele-sensitive reactions on the genetic material of the sample at the genetic locus to obtain at least two quantitative allele-indicative reaction values, each allele-indicative reaction value being indicative of the likely presence or absence of a particular allele defined with respect to the genetic locus, the reaction values corresponding to the sample being processed to form a reaction-value data point;

(b) associating one of the genotypic classes with the sample using the reaction-value data point corresponding to the sample to define a sample genotypic class;

(c) obtaining with respect to each of the genotypic classes corresponding reaction-value data-point conditional-probability-measure distribution information providing, over a set of hypothetical reaction-value data points, a conditional probability measure as a function of the hypothetical reaction-value data point given the genotypic class;

(d) evaluating the reaction-value data-point conditional-probability-measure distribution information corresponding to the genotypic class associated with the sample with respect to the reaction-value data point corresponding to the sample to obtain a reaction-value data-point conditional probability measure of the reaction-value data point given the sample genotypic class; and

(e) establishing a confidence measure for the association of the sample genotypic class with the sample using the reaction-value data-point conditional probability measure of the reaction-value data point given the sample genotypic class.

107. (new) The method according to claim 106 in which at least one genotypic class identifies a failed-experiment condition.

108. (new) The method according to claim 106 in which the confidence measure is an LOD score defining a confidence score.

109. (new) The method according to claim 108, further comprising the step of triggering an alarm condition upon detecting a statistically significant downward trend in confidence scores over time.

110. (new) The method according to claim 106 in which the allele-indicative reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, allele-specific hybridization, and allele-specific amplification, including such amplification by a polymerase chain reaction or a ligase chain reaction.

111. (new) The method according to claim 106 wherein processing the reaction values corresponding to the sample to form a reaction-value data point includes one or more of the steps of normalizing input data, subtracting background values from input data, and removing apparent outlier points.

112. (new) The method according to claim 106 wherein the step (c) of obtaining with respect to each genotypic class corresponding reaction-value data-point conditional-probability-measure distribution information comprises, for each genotype of the genotypic classes, fitting the reaction-value data-point conditional-probability-measure distribution information corresponding to the genotype to a subset of certain input data assumed to be of the genotypic class defined with respect to such genotype.

113. (new) A method according to claim 106, wherein the reaction values are measurements of an optical signal or a digital image intensity value.

114. (new) A method according to claim 106, wherein the reaction values are obtained by assaying for one or more alleles in genetic material from a subject that provide information relating to a trait.

115. (new) A method according to claim 106, wherein the reaction values are obtained by assaying for one or more alleles in genetic material from a subject that provide information pertaining to the identity or parentage of the subject.